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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=3; day=12; hr=16; min=29; sec=19; ms=664;]

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Application No: 10808758 Version No: 3.0

Input Set:

Output Set:

Started: 2008-02-27 21:36:38.302
Finished: 2008-02-27 21:36:44.860
Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 558 ms
Total Warnings: 119
Total Errors: 0
No. of SeqIDs Defined: 122
Actual SeqID Count: 122

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2008-02-27 21:36:38.302
Finished: 2008-02-27 21:36:44.860
Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 558 ms
Total Warnings: 119
Total Errors: 0
No. of SeqIDs Defined: 122
Actual SeqID Count: 122

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22) This error has occurred more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (33)
W 402	Undefined organism found in <213> in SEQ ID (34)
W 402	Undefined organism found in <213> in SEQ ID (35)
W 402	Undefined organism found in <213> in SEQ ID (36)
W 402	Undefined organism found in <213> in SEQ ID (37)
W 402	Undefined organism found in <213> in SEQ ID (38)
W 402	Undefined organism found in <213> in SEQ ID (39)
W 402	Undefined organism found in <213> in SEQ ID (40)

SEQUENCE LISTING

<110> The Scripps Research Institute
Von Seggern, Daniel J.

<120> ADENOVIRUS PARTICLES WITH ENHANCED INFECTIVITY OF DENDRITIC
CELLS AND PARTICLES WITH DECREASED INFECTIVITY OF HEPATOCYTES

<130> SCRIP1860-2

<140> 10808758
<141> 2004-03-24

<150> US 60/467,500

<151> 2003-05-01

<150> US 60/459,000

<151> 2003-03-28

<160> 122

<170> FastSEQ for Windows Version 4.0

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<212> DNA
<213> Adenovirus type 5

<220>
<221> CDS
<222> (1) ... (1743)

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1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc 96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 288
Gln Asn Val Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta			336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu			
100	105	110	
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc			384
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr			
115	120	125	
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att			432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile			
130	135	140	
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa			480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln			
145	150	155	160
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act			528
Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr			
165	170	175	
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg			576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu			
180	185	190	
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg			624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly			
195	200	205	
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act			672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr			
210	215	220	
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act			720
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr			
225	230	235	240
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca			768
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala			
245	250	255	
gga gga cta agg att gat tct caa aac aca aga cgc ctt ata ctt gat gtt			816
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val			
260	265	270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag			864
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln			
275	280	285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac			912
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn			
290	295	300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag			960
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu			
305	310	315	320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata			1008
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile			
325	330	335	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca			1056
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro			
340	345	350	
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat			1104
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp			
355	360	365	
tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac			1152
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp			
370	375	380	
agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act			1200
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr			
385	390	395	400
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag			1248
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu			
405	410	415	
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata			1296
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile			
420	425	430	
ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata			1344
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile			
435	440	445	
tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat			1392
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn			
450	455	460	
gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt			1440
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe			
465	470	475	480
aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga			1488
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly			
485	490	495	
ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc			1536
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala			
500	505	510	
aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa			1584
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys			
515	520	525	
cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac			1632
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp			
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aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc			1680

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<211> 581
<212> PRT
<213> Adenovirus type 5

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 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
 20 25 30
 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
 35 40 45
 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
 50 55 60
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
 65 70 75 80
 Gln Asn Val Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
 85 90 95
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
 100 105 110
 Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
 115 120 125
 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
 130 135 140
 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
 145 150 155 160
 Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
 165 170 175
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
 180 185 190
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
 195 200 205
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
 210 215 220
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225 230 235 240
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245 250 255
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
 260 265 270
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
 275 280 285
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
 290 295 300
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305	310	315	320
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile			
325	330	335	
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro			
340	345	350	
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp			
355	360	365	
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp			
370	375	380	
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr			
385	390	395	400
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu			
405	410	415	
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile			
420	425	430	
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile			
435	440	445	
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn			
450	455	460	
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe			
465	470	475	480
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly			
485	490	495	
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala			
500	505	510	
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys			
515	520	525	
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp			
530	535	540	
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly			
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His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser			
565	570	575	
Tyr Ile Ala Gln Glu			
580			

<210> 3
<211> 1746
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct: 5F KO1

<220>
<221> CDS
<222> (1)...(1743)

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tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc			96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro			
20	25	30	

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct		144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser		
35	40	45
ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc		192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu		
50	55	60
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc		240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser		
65	70	75
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac		288
Gln Asn Val Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn		
85	90	95
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta		336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu		
100	105	110
act gtg gct gcc gca cct cta atg gtc gcg ggc aac aca ctc acc		384
Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr		
115	120	125
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att		432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile		
130	135	140
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa		480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln		
145	150	155
160		
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act		528
Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr		
165	170	175
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg		576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu		
180	185	190
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg		624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly		
195	200	205
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act		672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr		
210	215	220
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act		720
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr		
225	230	235
240		
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca		768
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala		
245	250	255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt		816	
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val			
260	265	270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag		864	
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln			
275	280	285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac		912	
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn			
290	295	300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag		960	
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu			
305	310	315	320
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata		1008	
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile			
325	330	335	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca		1056	
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro			
340	345	350	
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat		1104	
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp			
355	360	365	
tca aac aag gct atg cct aaa cta gga act ggc ctt agt ttt gac		1152	
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp			
370	375	380	
agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act		1200	
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr			
385	390	395	400
ttg tgg acc aca cca gct cca gag gct aac tgt aga cta aat gca gag		1248	
Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu			
405			